

FIG. 1

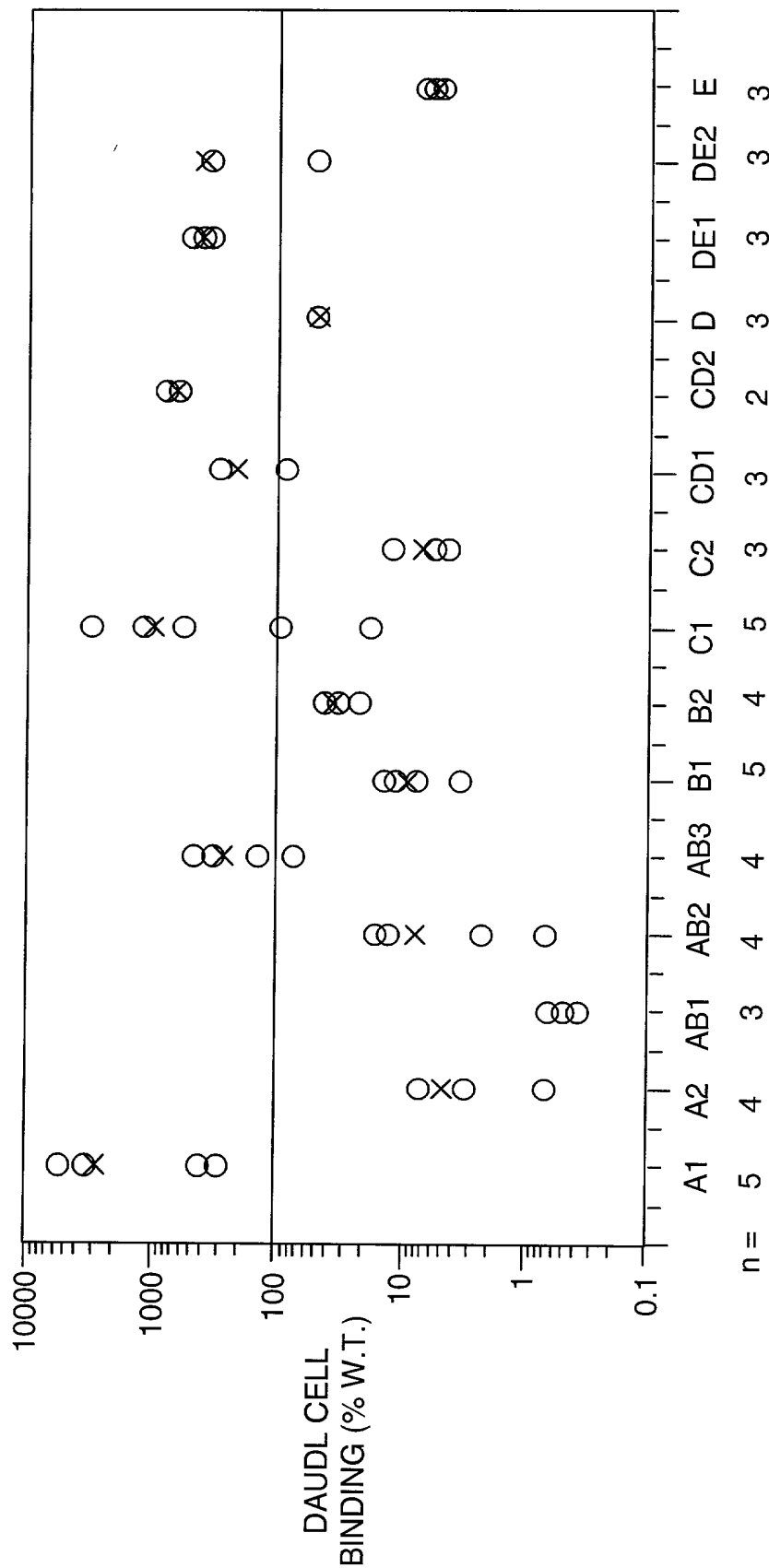


FIG. 2

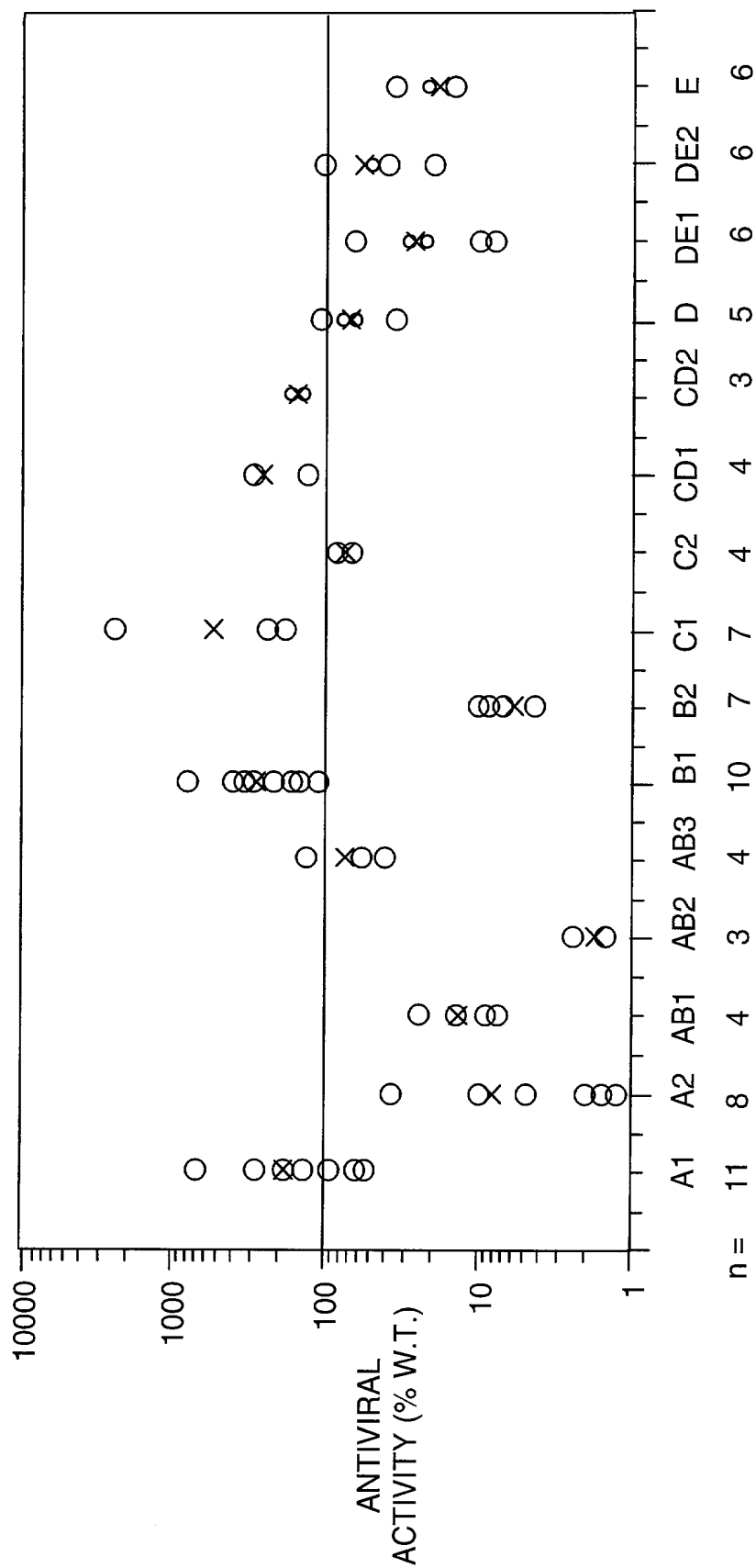


FIG. 3

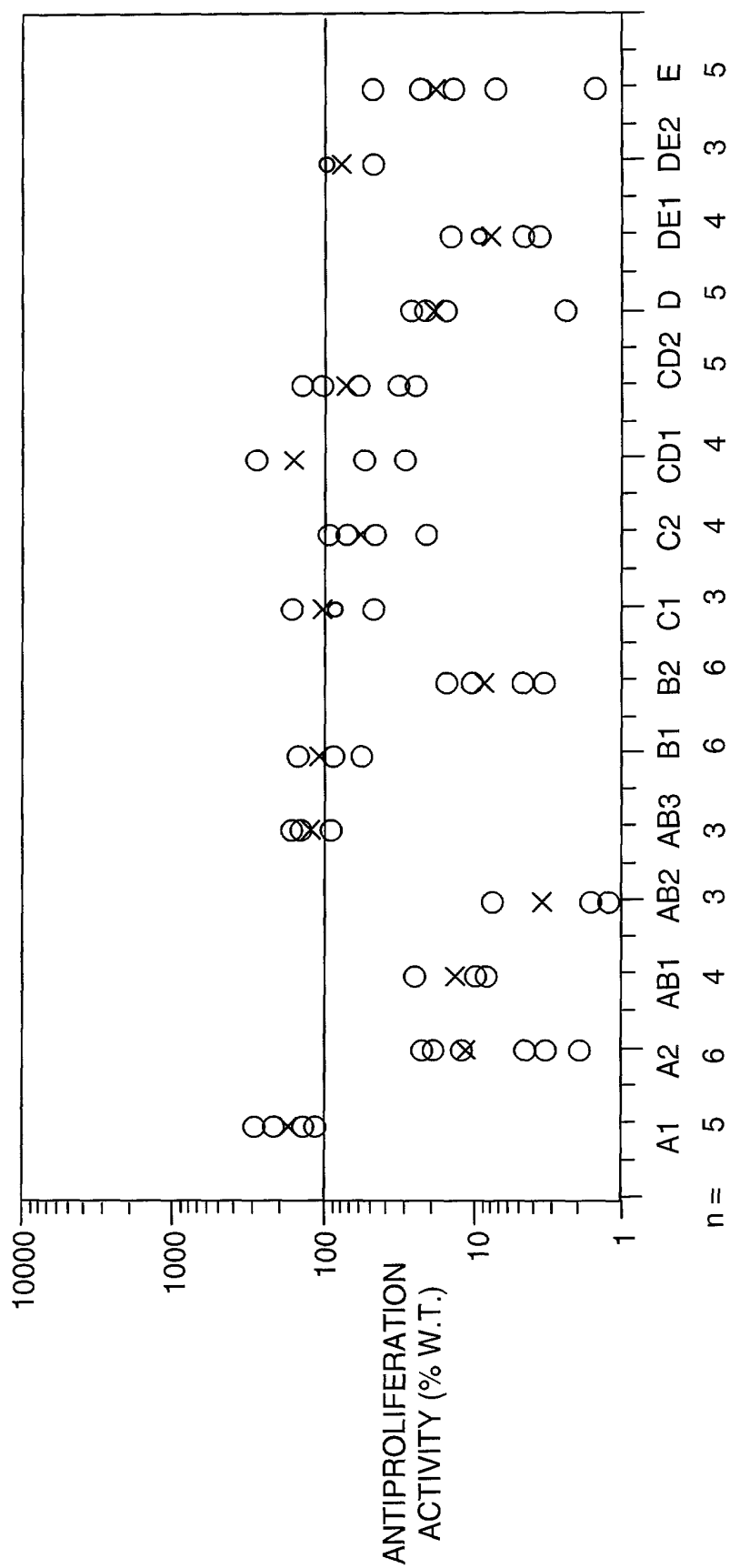


FIG. 4

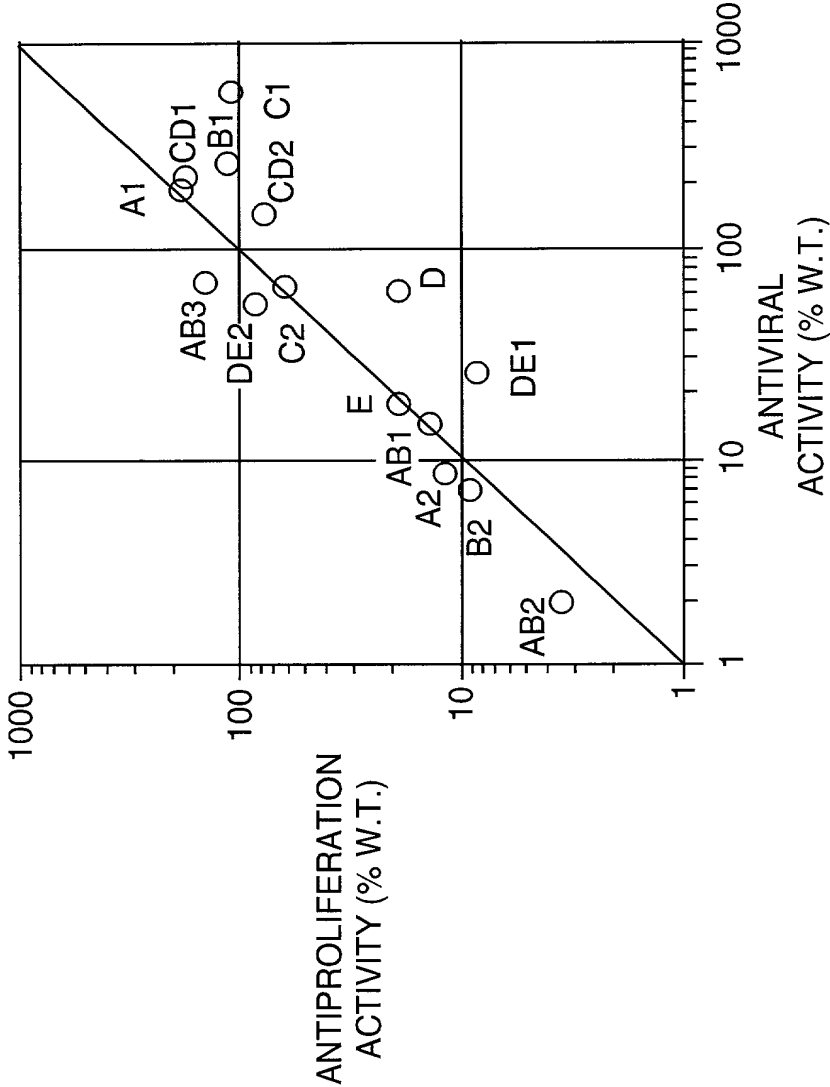
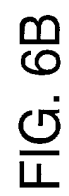
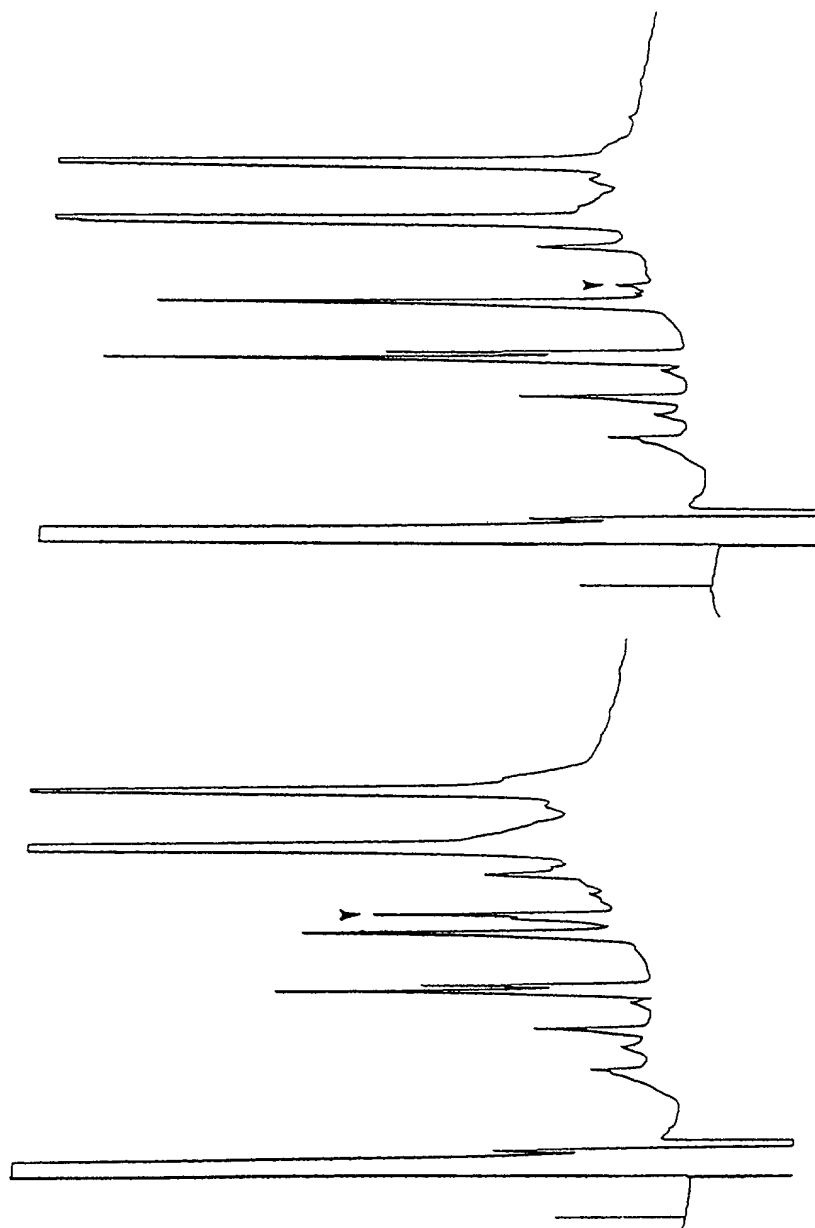


FIG. 5



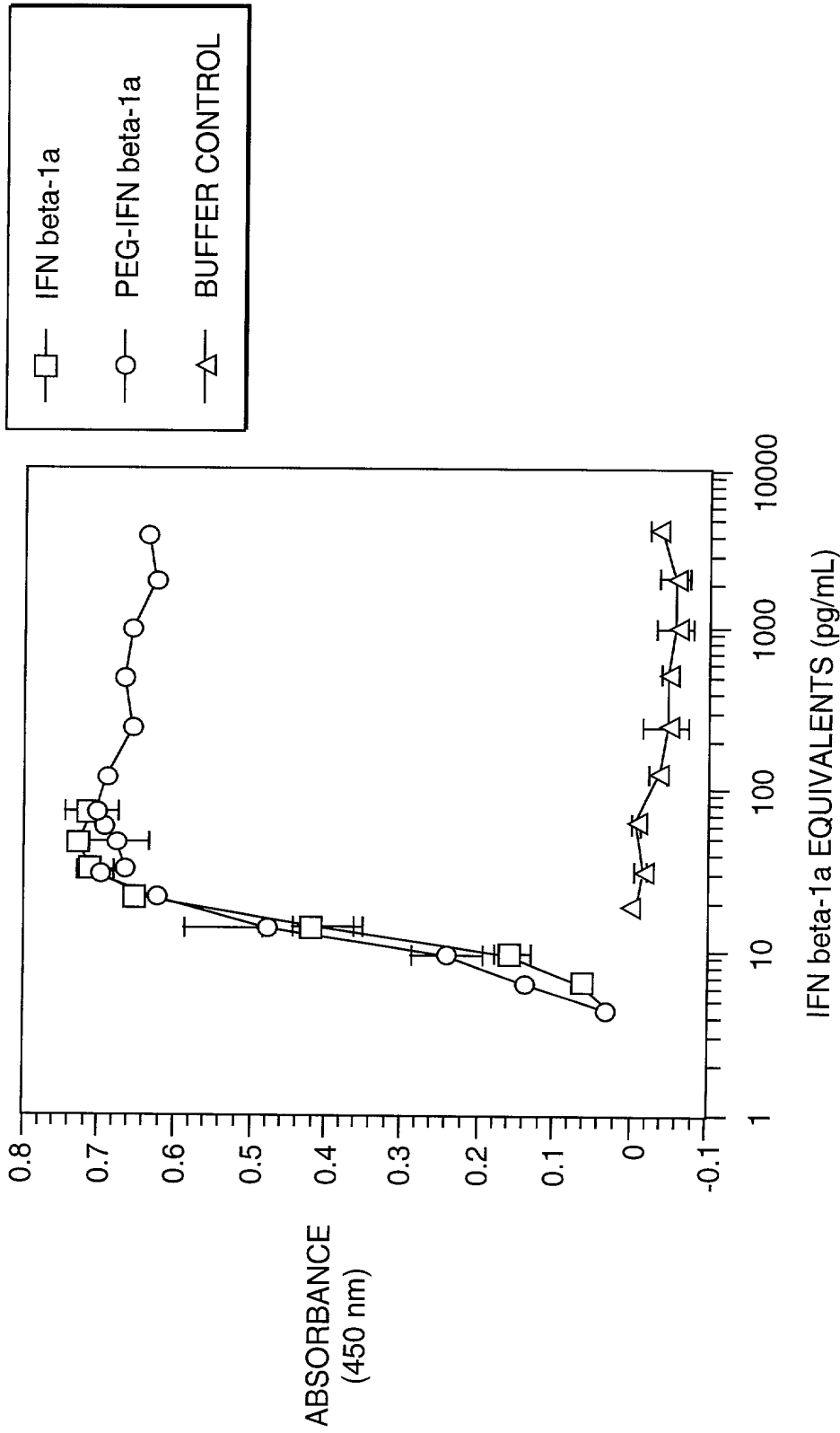


FIG. 7

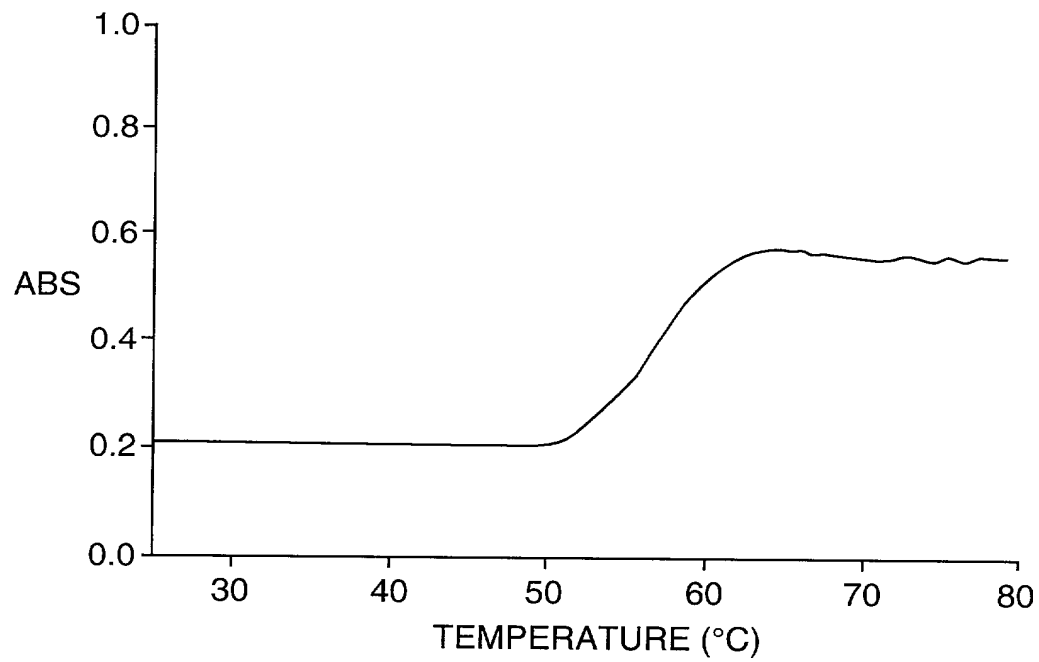


FIG. 8a

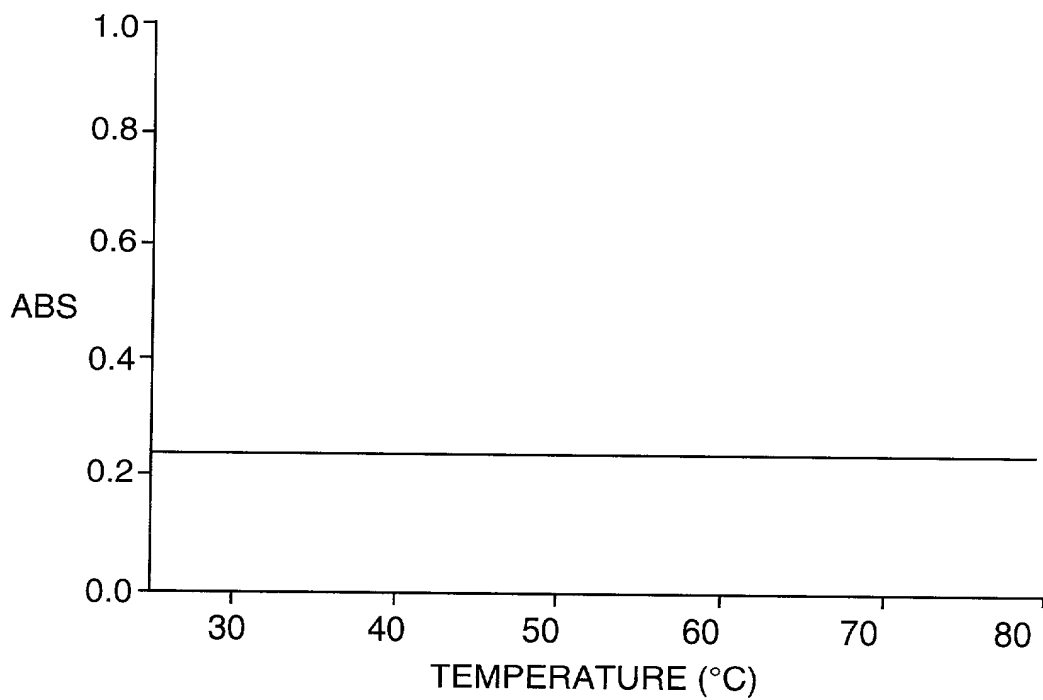


FIG. 8b



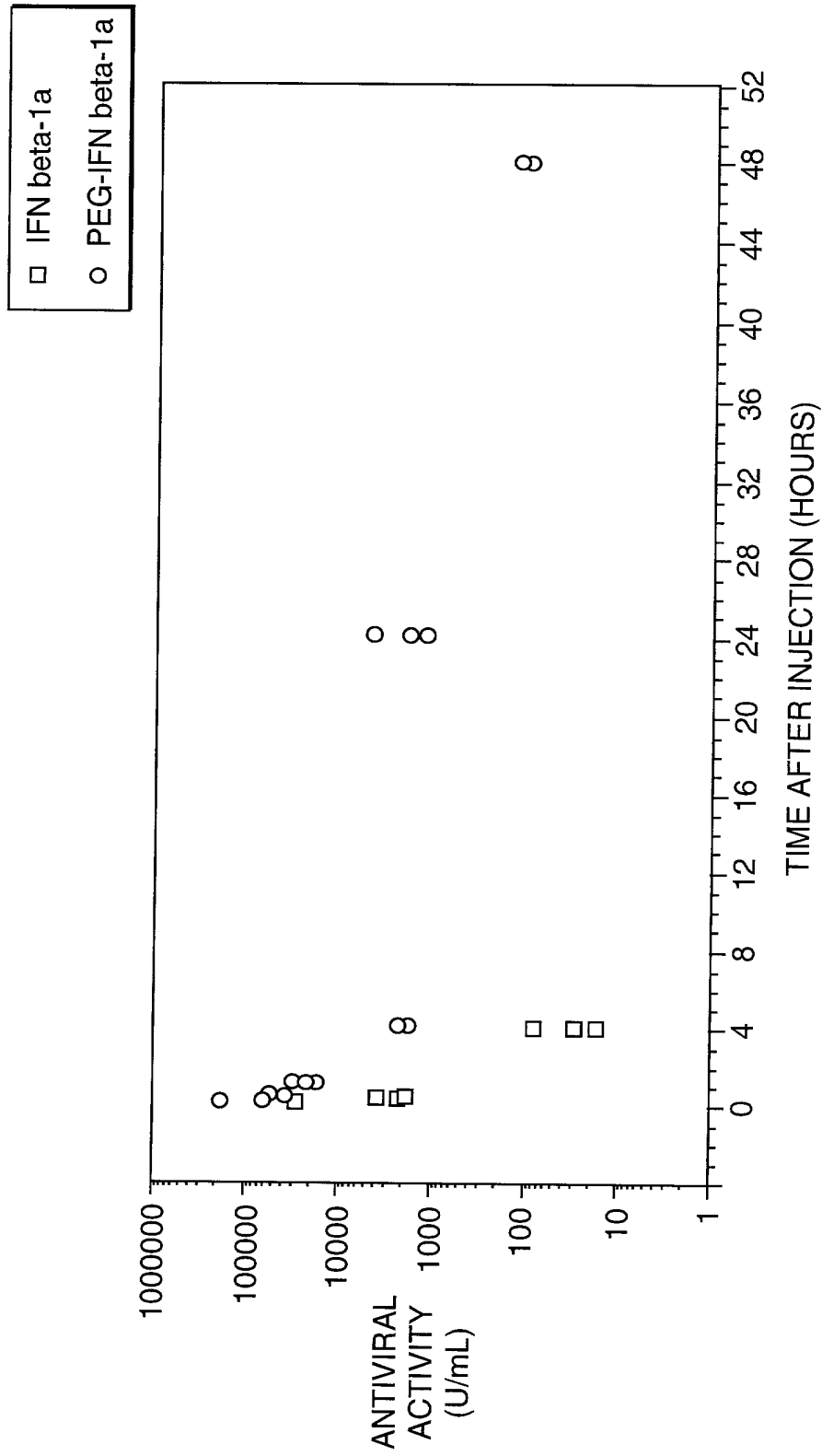


FIG. 9

1 TCCGGGGGCC ATCATCATCA TCATCATAGC TCCGGAGACG ATGATGACAA GATGAGCTAC  
 AGGCCCCCGG TAGTAGTAGT AGTAGTATCG AGGCCTCTGC TACTACTGTT CTA CTCTCGATG  
 1 ▶ Ser Gly Gly H i s H i s H i s H i s Ser Ser Gly Asp A s p Asp Asp Lys s Met Ser Tyr  
 61 AACTTGCTTG GATTCTTACA AAGAAGCAGC AATTTTCAGT GTCAGAAGCT CCTGTGGCAA  
 TTGAACGAAC CTAAGGATGT TTCTTCGTCG TTA AAAAGTCA CAGTCTTCGA GGACACCGTT  
 21 ▶ Asn Leu Leu G l y Phe Leu Gl n Ar g Ser Ser Asn Phe Gl n C ys Gl n Lys Le u Leu Tr p Gl n  
 121 TTGAATGGGA GGCTTGAATA CTGCCTCAAG GACAGGATGA ACTTTGACAT CCCTGAGGAG  
 AACTTACCCT CCGAACTTAT GACGGAGTTC CTGTCCTACT TGAAACTGTA GGGACTCCTC  
 41 ▶ Leu Asn Gly A r g Leu Gl u Ty r Cys Leu Lys Asp Ar g Met A sn Phe Asp l l e Pr o Gl u Gl u  
 181 ATTAAGCAGC TGCAGCAGTT CCAGAAGGAG GACGCCGCAT TGACCATCTA TGAGATGCTC  
 TAATTCGTCG ACGTCGTCAA GGTCTTCCTC CTGCGGCGTA ACTGGTAGAT ACTCTACGAG  
 61 ▶ l l e Lys Gl n L eu Gl n Gl n Ph e Gl n Lys Gl u Asp A l a A l a L eu Thr l l e Ty r Gl u Met Leu  
 241 CAGAACATCT TTGCTATTTT CAGACAAGAT TCATCTAGCA CTGGCTGGAA TGAGACTATT  
 GTCTTGTA A ACGATAAAA GTCTGTTCTA AGTAGATCGT GACCGACCTT ACTCTGATAA  
 81 ▶ Gl n Asn l l e P h e A l a l l e Ph e Ar g Gl n Asp Ser Ser Ser T hr Gly Tr p As n Gl u Thr l l e  
 301 GTTGAGAACC TCCTGGCTAA TGTCTATCAT CAGATAAACC ATCTGAAGAC AGTCCTGGAA  
 CAACTCTTGG AGGACCGATT ACAGATAGTA GTCTATTTGG TAGACTTCTG TCAGGACCTT  
 101 ▶ Val Gl u Asn L eu Leu A l a As n Val Tyr Hi s Gl n l l e Asn H i s Leu Lys Th r Val Leu Gl u  
 361 GAAAAACTGG AGAAAGAAGA TTTCAACCAGG GGAAAACTCA TGAGCAGTCT GCACCTGAAA  
 CTTTTTGACC TCTTTCTTCT AAAGTGGTCC CCTTTTGAGT ACTCGTCAGA CGTGGACTTT  
 121 ▶ Gl u Lys Leu G l u Lys Gl u As p Phe Thr Ar g Gly Lys Leu M et Ser Ser Le u Hi s Leu Lys  
 421 AGATATTATG GGAGGATTCT GCATTACCTG AAGGCCAAGG AGTACAGTCA CTGTGCCTGG  
 TCTATAATAC CCTCCTAAGA CGTAATGGAC TTCCGGTTCC TCATGTCAGT GACACGGACC  
 141 ▶ Ar g Tyr Tyr G l y Ar g l l e Le u Hi s Tyr Leu Lys A l a Lys G l u Tyr Ser Hi s Cys A l a Tr p  
 481 ACCATAGTCA GAGTGGAAAT CCTAAGGAAC TTTTACTTCA TTAACAGACT TACAGGTTAC  
 TGGTATCAGT CTCACCTTTA GGATTCCCTG AAAATGAAGT AATTGTCTGA ATGTCCAATG  
 161 ▶ Thr l l e Val A r g Val Gl u l l e Leu Ar g Asn Ph e Tyr Ph e l l e Asn Ar g Le u Thr Gly Tyr  
 541 CTCCGAAAC  
 GAGGCTTTG  
 181 ▶ Leu Ar g Asn

FIG. 10

